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Run on: May 12, 2003, 14:59:17 ; Search time 97 Seconds (without alignments)  
(1680.240 Million cell updates/sec)

Title: US-09-804-472-2

Perfect score: 4177  
Sequence: 1 MDASSDPYLPGGGDNPL.....DILRHMAQTANQDPASIMEN 791

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21;\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp Rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: SP\_rvirus:\*

16: sp\_bacteriop:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

17	1376	32.9	310	11	Q9WUG1	Q9wug1 cavia porce
18	1020.5	24.4	772	5	060958	060958 leishmania
19	1015	24.3	812	3	060159	060159 schizosacch
20	771	18.5	796	5	Q9BBH2	Q9bbh2 caenorhabdi
21	748.5	17.9	758	4	Q9UJH7	Q9ujh7 homo sapien
22	73.5	17.6	812	4	Q96RY8	Q96ry8 homo sapien
23	728	17.4	772	10	Q81491	Q81491 arabidopsis
24	728	17.4	792	10	P92943	P92943 arabidopsis
25	714.5	17.1	811	5	Q9U6W6	Q9u6w caenorhabdi
26	709	17.0	667	3	Q94287	Q94287 schizosacch
27	69.75	16.7	869	6	Q9TT16	Q9tt16 oryctolagus
28	69.2	16.6	813	5	Q9V6D9	Q9v6d9 dioscorea
29	684.5	16.4	764	10	P93567	P93567 solanum tub
30	681.5	16.3	1001	5	Q9BMK9	Q9bmk9 caenorhabdi
31	679	16.3	863	5	Q95VF8	Q95vf8 dictyostelium
32	676	16.2	780	10	P92942	P92942 arabidopsis
33	671.5	16.1	780	10	Q40485	Q40485 nicotiana
34	670.5	16.1	775	10	Q64990	Q64990 arabidopsis
35	669.5	16.0	775	10	Q93150	Q93150 arabidopsis
36	668.5	16.0	775	10	P92941	P92941 arabidopsis
37	667	16.0	779	10	Q96282	Q96282 arabidopsis
38	663	15.9	745	5	Q95QNB	Q95qn8 caenorhabdi
39	662	15.8	887	11	Q54822	Q54822 rattus norv
40	661	15.8	786	10	Q9XF71	Q9xf71 nicotiana
41	652	15.6	907	11	Q54821	Q54821 rattus norv
42	646.5	15.5	1084	5	Q9BMK8	Q9bmk8 caenorhabdi
43	646	15.5	1046	5	Q95ZP5	Q95zp5 caenorhabdi
44	645	15.5	1085	5	Q95ZP5	Q95zp5 caenorhabdi
45	645.5	15.5	773	10	Q96325	Q96325 arabidopsis

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15: SP\_rvirus:\*

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Database : SPTREMBL\_21;\*

1: sp\_archaea:\*

QY	3 ASSDPYLPYDGG-----DNPRLREHKRGHTYMTNGSINSSTHLLDDEPI 52	RA	Shimada K., Li X., Xu G., Nowak D.E., Shovalter L.A., Weinman S.A.,
DB	22 ASSDEEL-LDGAGVIMDQTSDEDDNL-LDGDTAFTGHTYMTNGSINSSTHLLDDEPI 79	RT	"Expression and canalicular localization of two isoforms of the CIC-3 chloride channel from rat hepatocytes";
QY	53 PGVGYDHFHTDWRECKDKERRRRINSKKRSEAMETKSLYDAWSGLWVLTGLAS 112	RL	Am. J. Physiol. Gastrointest. Liver Physiol. 279:G268-G276 (2000).
DB	80 PGVGYDHFHTDWRECKDKERRRRINSKKRSEAMETKSLYDAWSGLWVLTGLAS 139	DR	EMBL: AF142778; AAD2940.1; -
QY	113 GALAGLIDIADWMTDLKEGICLALSALWNHEOCWSNETTFFERDKCPQWTWAEILIG 172	DR	InterPro: IPR0044; PF00544; CDS_2.
DB	140 GALAGLIDIADWMTDLKEGICLALSALWNHEOCWSNETTFFERDKCPQWTWAEILIG 199	DR	InterPro: IPR0107; CL-channel_volt.
QY	173 QAEPPGSYIMNYIMYFWALSAFLAVSLVKGVPACGSGIPEKILSFGFIRGYLGK 232	DR	Pram: PF00571; CDS: 2.
DB	200 QAEPPGSYIMNYIMYFWALSAFLAVSLVKGVPACGSGIPEKILSFGFIRGYLGK 259	DR	PRINTS: PR00762; CLCHANNEL.
QY	233 WTLMIKITTIVLAVASLSLGKREGPLVHACCGNFSYLPKYSTNEAKKREVLASA 292	DR	SMART: SM00116; CBS: 2.
DB	260 WTLMIKITTIVLAVASLSLGKREGPLVHACCGNFSYLPKYSTNEAKKREVLASA 319	FT	NON_TER: 818; AA: 818
QY	293 AGVSVAFPIGGVLSLEEVSYYPKLTLWRSFAALVAFLVRSINPFGNSRLVLYFV 352	SEQUENCE	818 AA: 90854 MW: 0651441404AC6F CRC64;
DB	320 AGVSVAFPIGGVLSLEEVSYYPKLTLWRSFAALVAFLVRSINPFGNSRLVLYFV 379	QY	Query Match: 96.5%; Score: 4032; DB: 11; Length: 818;
QY	353 EYHTPWLFELPFPLLGVLGEGIWAFLVAKRNLKQEGIPLVHACCGNFSYLPKYSTNEAKKREVLASA 412	Best Local Similarity	96.7%; Pred. No. 3, 3e-318;
DB	380 EYHTPWLFELPFPLLGVLGEGIWAFLVAKRNLKQEGIPLVHACCGNFSYLPKYSTNEAKKREVLASA 439	Matches	773; Conservative: 4; Mismatches: 10; Indels: 12; Gaps: 3;
QY	413 VIAFPNPyTRINTSLLKELETFDCGPLESSLCYDYNMDNASKIVDIDPDRAGIVYSA 472	DB	3 ASSDPYLPYDGG-----DNPRLREHKRGHTYMTNGSINSSTHLLDDEPI 52
DB	440 VIAFPNPyTRINTSLLKELETFDCGPLESSLCYDYNMDNASKIVDIDPDRAGIVYSA 499	QY	22 ASSDEEL-LDGAGAIMDQTSDEDDNL-LDGDTAFTGHTYMTNGSINSSTHLLDDEPI 79
QY	473 IWOLCLALIFKIMTVEFGIKVPSGLFIPSMAGAIGAIGRIVGIAVEQLAYVHDMIFIK 532	DB	53 PGVGYDHFHTDWRECKDKERRRRINSKKRSEAMETKSLYDAWSGLWVLTGLAS 112
DB	500 IWOLCLALIFKIMTVEFGIKVPSGLFIPSMAGAIGAIGRIVGIAVEQLAYVHDMIFIK 559	QY	80 PGVGYDHFHTDWRECKDKERRRRINSKKRSEAMETKSLYDAWSGLWVLTGLAS 139
QY	533 EWCVEGADCTPGLYAMGAACLGGSYRMTWLSVWIVFELTGGLEYIVPMAMVTSK 592	DB	80 PGVGYDHFHTDWRECKDKERRRRINSKKRSEAMETKSLYDAWSGLWVLTGLAS 139
DB	560 EWCVEGADCTPGLYAMGAACLGGSYRMTWLSVWIVFELTGGLEYIVPMAMVTSK 619	QY	200 QAEPPGSYIMNYIMYFWALSAFLAVSLVKGVPACGSGIPEKILSFGFIRGYLGK 259
QY	593 VGDAGREGIYEAHIRLINGYFPLDAKEEFTHTTLAADMVRPDRNDPPLAVLTODNMVDD 652	DB	233 WTLMIKITTIVLAVASLSLGKREGPLVHACCGNFSYLPKYSTNEAKKREVLASA 292
DB	620 VGDAGREGIYEAHIRLINGYFPLDAKEEFTHTTLAADMVRPDRNDPPLAVLTODNMVDD 679	QY	260 WTLMIKITTIVLAVASLSLGKREGPLVHACCGNFSYLPKYSTNEAKKREVLASA 319
QY	653 IENMINETSYNQFPVIMSKESORLWGFALRDLTAEISARKKQEGIVGSSRVCAQHTP 712	DB	293 AGVSVAFPIGGVLSLEEVSYYPKLTLWRSFAALVAFLVRSINPFGNSRLVLYFV 352
DB	680 IENMINETSYNQFPVIMSKESORLWGFALRDLTAEISARKKQEGIVGSSRVCAQHTP 739	DB	320 AGVSVAFPIGGVLSLEEVSYYPKLTLWRSFAALVAFLVRSINPFGNSRLVLYFV 379
QY	713 SLPAESPRPLKRSILDMSPTVTDITPMEIVVDFRKLGLRQCLVTHNGRLLGITKKD 772	QY	413 VIAFPNPyTRINTSLLKELETFDCGPLESSLCYDYNMDNASKIVDIDPDRAGIVYSA 472
DB	740 SLPAESPRPLKRSILDMSPTVTDITPMEIVVDFRKLGLRQCLVTHNGRLLGITKKD 799	DB	440 VIAFPNPyTRINTSLLKELETFDCGPLESSLCYDYNMDNASKIVDIDPDRAGIVYSA 499
QY	773 ILRHMQATANDOPASIMFN 791	QY	473 IWOLCLALIFKIMTVEFGIKVPSGLFIPSMAGAIGAIGRIVGIAVEQLAYVHDMIFIK 532
DB	800 ILRHMQATANDOPASIMFN 818	DB	500 IWOLCLALIFKIMTVEFGIKVPSGLFIPSMAGAIGAIGRIVGIAVEQLAYVHDMIFIK 559
<b>RESULT 2</b>			
OXR287	PRELIMINARY; PRT: 818 AA.	QY	533 EWCVEGADCTPGLYAMGAACLGGSYRMTWLSVWIVFELTGGLEYIVPMAMVTSK 592
ID	09R287	DB	560 EWCVEGADCTPGLYAMGAACLGGSYRMTWLSVWIVFELTGGLEYIVPMAMVTSK 619
AC	09R287;	QY	593 VGDAGREGIYEAHIRLINGYFPLDAKEEFTHTTLAADMVRPDRNDPPLAVLTODNMVDD 652
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DB	620 VGDAGREGIYEAHIRLINGYFPLDAKEEFTHTTLAADMVRPDRNDPPLAVLTODNMVDD 679
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	QY	653 IENMINETSYNQFPVIMSKESORLWGFALRDLTAEISARKKQEGIVGSSRVCAQHTP 712
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DB	680 IENMINETSYNQFPVIMSKESORLWGFALRDLTAEISARKKQEGIVGSSRVCAQHTP 739
OS	Chloride channel protein 3 long form (Fragment).	QY	713 SLPAESPRPLKRSILDMSPTVTDITPMEIVVDFRKLGLRQCLVTHNGRLLGITKKD 772
OC	Rattus norvegicus (Rat).	DB	740 SLPAESPRPLKRSILDMSPTVTDITPMEIVVDFRKLGLRQCLVTHNGRLLGITKKD 799
OC	Rattus norvegicus (Rat).	QY	773 ILRHMQATANDOPASIMFN 791
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	DB	800 ILRHMQATANDOPASIMFN 818
NCBI_TaxId=10116;			
SEQUENCE FROM N_A.			
RP	STRAIN=SPRAGUE-DALEY;		
RC	MEDLINE=20378002; PubMed=10915634;		
RX			

RESULT 3		Db	181	SGIPEIKITILSGFIFTIYLGKNTLMTKTTIVLAVASGLSGKKEPLVHACCGNFSY	240
018894	PRELIMINARY;	QY	272	LFPKYSTNEAKKREVLSAASAGVSVAFGA,PIGGVIFSLSEVSYFPLKTLWRSFFALV	331
ID		Db	241	UFPKYSTNEAKKREVLSAASAGVSVAFGA,PIGGVIFSLSEVSYFPLKTLWRSFFALV	300
AC					
018894;					
DT	01-JAN-1998 (Tremblrel. 05, Created)	QY	332	AAPVLRINSNPFGNSRLVLFVWYHTPWFEL,FPFTLGVVGLWMAFFIRANIA,CCR	391
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)	Db	301	AAFLVLRINSNPFGNSRLVLFVWYHTPWFEL,FPFTLGVVGLWMAFFIRANIA,CCR	360
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)				
DE	Chloride channel protein 3 (CLC-3).				
GN					
OS	Oryctolagus cuniculus (Rabbit)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX					
RN	[1]				
RP	SEQUENCE FROM N. A.				
RC	STRAIN-NEW ZEALAND WHITE; TISSUE=CORNEAL ENDOTHELIUM;				
RA	Rae J. L.; Shepard A. R.;				
RL	Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE				
CC	SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;				
CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND				
CC	TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL				
CC	CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY				
CC	PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-				
CC	TERM MEMORY (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-!- SIMILARITY: TO OTHER CHLORIDE CHANNELS.				
DR	EMBL; AF02348; AAB95163.1; ALT-INIT.	QY	572	ELTGGLYIVPLMAAWTSKWGA,FGREGYIEAHRLNGYPLDAKEEFTT,LAADM	631
DR	InterPro; IPR00644; CBS_domain.	Db	541	ELTGGLYIVPLMAAWTSKWGA,FGREGYIEAHRLNGYPLDAKEEFTT,LAADM	600
DR	InterPro; IPR01807; Cl-channel_volt.		481	RTVGLAVEOLATYHDMWTFKEMCEVGA,DC,TPGLYAMVGAACLGVTWVSLAVIE	540
DR	InterPro; PF0051; CBS; 2.		601	RFRNDPPLAVLTDQNMVTDENMINETSYNGFPVIMSKESQRLYGFALKRDTAIES	660
DR	Pfam; PF0054; voltage_CLC; 1.		692	ARKKQESIVGSSRVCFQHTSPSPRPLRSILMSPEVTHTPMELVVD,FRKL	751
DR	PRINTS; PRO0762; CLCHANNEL.		661	ARKKQEGIVGSSRVCFQHTSPSPRPLRSILMSPEVTHTPMELVVD,FRKL	720
KW	SMART; SM00116; CBS; 2.		752	GLRQCLVTHNSRLGLITKTDLRLHMQTAQNDPASIMFN	791
KW	Ionic channel; Ion transport; voltage-gated channel; Transmembrane;		721	GLUQCLVTHNGLIGLITKKDILRLHMQTAQNDPASIMFN	760
FT	CBS domain.				
FT	TRANSMEM 68	QY	154	POTENTIAL.	
FT	TRANSMEM 175	QY	174	POTENTIAL.	
FT	TRANSMEM 195	QY	222	POTENTIAL.	
FT	TRANSMEM 202	QY	2279	POTENTIAL.	
FT	TRANSMEM 259	QY	305	POTENTIAL.	
FT	TRANSMEM 330	QY	350	POTENTIAL.	
FT	TRANSMEM 365	QY	385	POTENTIAL.	
FT	TRANSMEM 442	QY	462	POTENTIAL.	
FT	TRANSMEM 467	QY	487	POTENTIAL.	
FT	TRANSMEM 508	QY	528	POTENTIAL.	
FT	TRANSMEM 536	QY	556	POTENTIAL.	
FT	DOMAIN 577	QY	616	CBS 1.	
FT	DOMAIN 698	QY	749	CBS 2.	
SQ	SEQUENCE 760 AA:	DB	84516	MW:	9B6DDA86296847E7 CRC64:
Query Match	95.8%; Score 4002; DB 6; Length 760;				
Best Local Similarity	100.0%; Pred. No. 8.8e-316; Indels 0; Gaps 0;				
Matches 760;	Conservative 0; Mismatches 0;				
OY	32 MTNGGSINSSTHLLDILEPIPGVSYDDFTITDWRKREKCDRERHRINNSKKKSAEW 91	QY	09YH11	PRELIMINARY;	PRT; 791 AA.
Db	1 MTNGGSINSSTHLLDILEPIPGVSYDDFTITDWRKREKCDRERHRINNSKKKSAEW 60	DR	01-MAY-1999 (Tremblrel. 10, Created)		
DR	EMBL; Y0941; CAA71072.2; -.	DR	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DR	InterPro; IPR00644; CBS_domain.	DR	01-JUN-2002 (Tremblrel. 21, Last annotation update)		
DR	InterPro; IPR01807; Cl-channel_volt.				
DR	Pfam; PF0051; CBS; 2.				
DR	PRINTS; PRO0762; CLCHANNEL.				
DR	SMART; SM00116; CBS; 2.				
RN	[1]				
RP	SEQUENCE FROM N. A.				
RC	TISSUE-DISTAL NEPHRON;				
RA	Lindenthal S. M. B.;				
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; Y0941; CAA71072.2; -.				
DR	InterPro; IPR00644; CBS_domain.				
DR	InterPro; IPR01807; Cl-channel_volt.				
DR	Pfam; PF0051; CBS; 2.				
DR	PRINTS; PRO0762; CLCHANNEL.				
DR	SMART; SM00116; CBS; 2.				
SQ	SEQUENCE 791 AA:	DB	88140	MW:	216B1B1ED2A8C4EA CRC64:
Query Match	95.6%; Score 3993; DB 13; Length 791;				
Best Local Similarity	94.2%; Pred. No. 5e-315; Indels 0; Gaps 0;				
Matches 745;	Conservative 26; Mismatches 20;				
OY	1 MTASSDPPYLPDGGSNIPPLREBLHKRGTHYNTGGSINSSTHLLDILEPIPGVSYDD	QY	1	MDISSDPYLPDGGSNIPPLREBLHKRGTHYNTGGSINSSTHLLDILEPIPGVSYDD	60
Db	1 MTSSDPPYLPDGGSNIPPLREBLHKRGTHYNTGGSINSSTHLLDILEPIPGVSYDD 60				
OY	212 SGIPERITLGSFINGYLGWLTMIKTTIVLAVASGLSLGKKEPLVHACCGNFSY 271				
Db	1 MDISSDPYLPDGGSNIPPLREBLHKRGTHYNTGGSINSSTHLLDILEPIPGVSYDD 60				

QY	61	FHIDWWRKCKDRERHRRNKSNSKESAMENTKSLYDASOSLWVILTGASGLAQLID
Db	61	FHIDWWRKCKDRERHRRNKSNSKESAMENTKSLYDASOSLWVILTGASGLAQLID
QY	121	IAADWMTDLREGICLISALWYHNEOCQCGWSNETTEFRDKCPOWKTWAEELITQGAEGPSY
Db	121	IAADWMTDLREGICLISALWYHNEOCQCGWSNETTEFRDKCPOWKTWAEELITQGAEGPSY
QY	181	IMWYIMYFWALSAFLAVSLVVKFAPYCGSGIEPEIKTILSGEIRGKGWTLMKTI
Db	181	IMWYIMYFWALSAFLAVSLVVKFAPYCGSGIEPEIKTILSGEIRGKGWTLMKTI
QY	241	TULAVASGLSLSLGEPLVHACCGNNTSYLPKYSTNEAKKREVELSAAAGVSFG
Db	241	TULAVASGLSLSLGEPLVHACCGNNTSYLPKYSTNEAKKREVELSAAAGVSFG
QY	301	APIGVVLFSLEEVYYFPKTLWRSFFAFLVAFAVFLRSINPGNSRLVFLVKEIHPWL
Db	301	APIGVVLFSLEEVYYFPKTLWRSFFAFLVAFAVFLRSINPGNSRLVFLVKEIHPWL
QY	361	FELFPFELIGVFGGLWGAFFRANAWCRRKSTFGKYPLEVIVALTAVIAPNPY
Db	361	FELFPFELIGVFGGLWGAFFRANAWCRRKSTFGKYPLEVIVALTAVIAPNPY
QY	421	TRNTESELKELFDGPPRESSLDYRNMSATVDDPDRPAGIVGIAVFLRSINPGNSRLVFLVKEIHPWL
Db	421	TRNTESELKELFDGPPRESSLDYRNMSATVDDPDRPAGIVGIAVFLRSINPGNSRLVFLVKEIHPWL
QY	481	IFLIMTMTFGIKVPSGLFIPSMAGATAFRIVTIAVEOLAYHHDWFLKEWCVEGAD
Db	481	IFLIMTMTFGIKVPSGLFIPSMAGATAFRIVTIAVEOLAYHHDWFLKEWCVEGAD
QY	541	CITPGLYAMVGAACLGSTTRMTVSLVIVFELTGGLEYIVPLMAVWMTSKWGDAGRE
Db	541	CITPGLYAMVGAACLGSTTRMTVSLVIVFELTGGLEYIVPLMAVWMTSKWGDAGRE
QY	601	GIVEAHIRNGYPLDAKEEFTHTLADDMRPRNDPPLAVLQMLVHDDWFLKEWCVEGAD
Db	601	GIVEAHIRNGYPLDAKEEFTHTLADDMRPRNDPPLAVLQMLVHDDWFLKEWCVEGAD
QY	661	SYNFPVNTKESORLVGALARROLTIALESARKKQEGTYGSSRVCFAQHPTSLPAPESP
Db	661	SYNFPVNTKESORLVGALARROLTIALESARKKQEGTYGSSRVCFAQHPTSLPAPESP
QY	721	PIKRSILMSPFVTDHPMEIWVDIFRKLGLRQCLVLYINGRGLIITKDKILRIMAQT
Db	721	PIKRSILMSPFVTDHPMEIWVDIFRKLGLRQCLVLYINGRGLIITKDKILRIMAQT
QY	781	ANODPASIMFN 791
Db	781	ANHDPESTLFN 791
RESULT 5		
P97274		
ID	P97274	PRELIMINARY, PRT, 760 AA.
AC	P97274;	
DT	01-MAY-1997 (TREMBLRE, 03, Created)	
DT	01-NOV-1999 (TREMBLRE, 12, Last sequence update)	
DT	01-JUN-2002 (TREMBLRE, 21, Last annotation update)	
DE	Volume-regulated outwardly-rectifying chloride channel.	
GN	CIC-3.	
OS	Cavia porcellus (Guinea Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystericognathi; Caviidae; Cavia.	
OX	NCBI_TaxID=10141;	
[1]	SEQUENCE FROM N.A.	
RP	MDDLINE=98009352; PubMed=93939484;	
RX	Duan D., Winter C., Cowley S., Hume J.R., Horowitz B.;	
RT	"Molecular identification of a volume-regulated chloride channel.";	
RL	Nature 390:417-421(1997).	

RNR  
 [2]  
 RRP  
 SEQUENCE FROM N.A.  
 Duan D., Winter C., Hume J.R., Horowitz B.;  
 Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 EMBL: U83464; AAC88634; 2; -  
 InterPro: IPR00644; CBS\_domain.  
 InterPro: IPR00807; C1\_channel\_volt.  
 Pfam: PF00571; CBS; 2;  
 Pfam: PF0054; voltage\_CLC; 1.  
 PRINTS: PRO0762; CLCHANNEL.  
 SMART: SM00116; CBS; 2;  
 SEQUENCE 760 AA; 84357 MW; DF8D017D1881A531 CRC64;  
 Best Local Similarity 95.4%; Score 3384; DB 11; Length 760;



Db	420	AGGIVSRSWQWQALITLIRKIVTITFQMKRIFSGLFIPSMAVGAIGRLGQHMEQLAY	479
Qy	525	HHDWFIFKEWCCEVGACDITPGLYAMGAAACIGGGVTTMVTSLVUVFELTGLEYIVPLM	584
Db	480	HHDWAIFNSWCSQGADCITPGLYAMGAAACIGGGVTTMVTSLVUVFELTGLEYIVPLM	539
Qy	585	RAVMTSKWQDAGREGSIVYEAHRLNGYPLFEKEETHITLADWMPRRNPPPLAVL	644
Db	540	AAAMTSKWAQDAGREGSIVYEAHRLNGYPLFEKEETHITLADWMPRRNPPPLAVL	599
Qy	645	QDNMTVDIENMINETSYNGFPVMSKESQRLVGFALRRDTIAESARKKOBGIVSSR	704
Db	600	QDSMTVEDVETISETTYSGFPVMSKESQRLVGFALRRDTIAESARKKOBGIVSSR	659
Qy	705	VCAQHTSLPAESPRPLKRSILDMSPTFTVHTPMIIVDIFRKIGLROCLVTHNRL	764
Db	660	IVFTEHSPMPYPTPTKLNRNLDSPFTVTDLTPMELIVDIFRKIGLROCLVTHNRL	719
Qy	765	LGITTKDILRHAQTANQDPSIMEN	791
Db	720	LGITTKDILRHAQTANQDPSILFN	746
RESULT 8			
Q9TTU3	PRELIMINARY;	PRT;	746 AA.
ID	Q9TTU3		
AC	09TTU3;		
DT	01-MAY-2000 (TREMBLEL, 13, Created)		
DT	01-JUN-2002 (TREMBLEL, 21, Last annotation update)		
DE	Chloride channel CLC-5.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID:9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEA EPITHELIUM;		
RA	Rae J.I.;		
RT	"Ion channels in Cornea Epithelia.";		
RL	Submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF195523; AAF06018.1; -.		
DR	InterPro; IPR00644; CBS domain.		
DR	InterPro; IPR001807; CL-channel_volt.		
DR	Pfam; PF00571; CBS; 2.		
DR	PRINTS; PRO0762; CLCHANNEL.		
DR	SMART; SM00116; CBS; 2.		
DR	SEQUENCE 746 AA; 83206 MW;	667F2701COBF06A CRC64;	
Query Match			
Best Local Similarity	75.3%	Score	3145.5;
Pred.	No. 2.5-	Length	746;
Matches	575;	Conservative	84;
	Mismatches	87;	Indels
	1;	Gaps	1;
RESULT 9			
Q9P66	PRELIMINARY;	PRT;	746 AA.
ID	Q9P66		
AC	Q9P66;		
DT	01-JUN-2001 (TREMBLEL, 17, Created)		
DT	01-JUN-2002 (TREMBLEL, 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLEL, 21, Last annotation update)		
DE	Chloride channel CICN5.		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBL_TaxID=10141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RT	Cornejo T., Cid L.P., Sepulveda F.V.;		
RT	"Cloning and Intestinal expression of guinea pig CIC-5 chloride channel.";		
RT	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF326998; AAG49580.1; -.		
DR	InterPro; IPR000544; CBS_domain.		
DR	InterPro; IPR001807; CL-channel_volt.		
DR	Pfam; PF00571; CBS; 2.		
DR	PRINTS; PRO0762; CLCHANNEL.		
DR	SMART; SM00116; CBS; 2.		
DR	SEQUENCE 746 AA;	83093 MW;	92FC8AFDC7D8D4A5 CRC64;
Query Match			
Best Local Similarity	74.4%	Score	3109.5;
Pred.	No. 2.1e-243;	Length	746;
Matches	569;	Conservative	88;
	Mismatches	89;	Indels
	1;	Gaps	1;
Qy	45	LDDLEDEPIPGVGTYDDFTIDWRECKDRERHRRNKKSKKESAWEMTSKLYDAWSCLW	104
Db	1	MDFLEEPIPGVGTYDDFTIDWRECKDRERHRRNKKSKKESAWEMTSKLYDAWSCLW	60
Qy	105	WLTGLASLAGLAGLIDIAADMWTDLKEGICLCSALWNHEQCGWSNETTFFERDKCPOWK	164
Db	61	MULIGFSGSLAGLIDIAADMWTDLKEGICLCSALWNHEQCGWSNETTFFERDKCPOWK	120
Qy	225	IRGYLGKWLMIKTTLVLAVASGLSLGKECPLVHVACCGCNIFSYLPKYSTNEAKR	284
Qy	165	TWAELITQGQSCPGPSYIMNYIWFALSAFLAVSLVLUVKVAPYAGSGGIREBIKTLSF	224
Db	121	SWSLQINTDECAFATIVNPFYVLUVLAFLAVSLVLUVKVAPYAGSGGIREBIKTLSF	180
Qy	285	EVLSAASAAGSVSVAFGAPIGGYLFLSEVSYEPLKTLWRSFFAALVAFAVLRSLPFGN	344
Qy	241	EYLSRARAAGVSTAFGAFIGGVFESERSYEPLKTLWRSFFAALVAFAVLRSLPFGN	300
Qy	345	SRIVLFVVEYHTPWYFELPFPLGIVGFGMCAFFRANIACCRKKSTKFGKPYVILE	404
Db	301	HHDWIFIFKWCCEVGACDITPGLYAMGAAACIGGGVTTMVTSLVUVFELTGLEYIVPLM	539
Qy	405	LIVAITAVAFNPPRNTSELEKEFHTDCPLESSLICRNDMASKIVDDPPLAVL	454
Db	361	LIVAITAVAFNPPRNTSELEKEFHTDCPLESSLICRNDMASKIVDDPPLAVL	419
Qy	445	AGIGVSYSATWOLCLALIFKIMTFTEGKVPGLFIPSMAIGAIGRIVGIAVEQLAY	524
Db	420	AGVQYNAWMOLALIILIKIVTITFQMKIPLSGLFIPSMAVGAIALAGLIGQHMEQLAY	479
Qy	525	HHDWFIFKWCCEVGACDITPGLYAMGAAACIGGGVTTMVTSLVUVFELTGLEYIVPLM	584
Db	480	HHDWIFIFKWCCEVGACDITPGLYAMGAAACIGGGVTTMVTSLVUVFELTGLEYIVPLM	539
Qy	585	RAVMTSKWQDAGREGSIVYEAHRLNGYPLFEKEETHITLADWMPRRNPPPLAVL	644
Db	600	QDSMTVEDVETISETTYSGFPVMSKESQRLVGFALRRDTIAESARKKOBGIVSSR	659
Qy	645	QDNMTVDIENMINETSYNGFPVMSKESQRLVGFALRRDTIAESARKKOBGIVSSR	704
Db	645	AAAMTSKWAQDAGREGSIVYEAHRLNGYPLFEKEETHITLADWMPRRNPPPLAVL	599
Qy	705	VCAQHTSLPAESPRPLKRSILDMSPTFTVHTPMIIVDIFRKIGLROCLVTHNRL	764
Db	660	IVFTEHSPMPYPTPTKLNRNLDSPFTVTDLTPMELIVDIFRKIGLROCLVTHNRL	719
Qy	765	LGITTKDILRHAQTANQDPSIMEN	791
Db	720	LGITTKDILRHAQTANQDPSILFN	746

Db	61 MLLIGLSSLAGLIDISAIWMTDKEGICTEGVFNHEICWMSQQVIFEDRKCPENN	120	DR Pfam: PF00654; voltage_CIC; 1.
Qy	165 TWAELIIGQAEGPSYIMNYIMYIWALSFPAFLAVSLVKAFCYAPCGSGIPEIKTILSGF	224	DR PRINTS; PRO0762; CICCHANNEL.
Db	121 SWSQILINNMDEGAFAKIVNYFMYWALLEAFLAVSLVKFAPYCGSGIPEIKTILSGF	180	DR SMART; SM0116; CBS; 2.
Qy	225 TIRGLGKWLMIKITYLVAWASGLSGKEGVPHVACCGNFFPSYLPKSYNEAKER	284	DR PROSITE; PS01137; TATD_1; UNKNOWN_1.
Db	181 TIRGLGKWLMIKITYLVAWASGLSGKEGVPHVACCGNFFPSYLPKSYNEAKER	240	DR SEQUENCE; 808 AA; 90068 MW; C3FTADC759BD1676 CRC64;
Qy	285 EVLSRASAAGSVAFAGPAGVFLSLEEVSYFPLKTMRSFFAFLVAFLVRSINPFGN	344	SQ
Db	241 EVLSRASAAGSVAFAGPAGVFLSLEEVSYFPLKTMRSFFAFLVAFLVRSINPFGN	300	Qy 22 ELHKRGTHYMT-----NGGSINSSHLDLDEPICGVYDDHTI 64
Qy	345 SRLVVFYVEHTPWLFELPFILGVFGLWGFIRANIAWRKSTKFGKPYVILEV	404	Db 25 EITEATLDFMTDOPPIDMAFGVUSINGNLNGAKVMDFLD--VPGVGTIEDFNTI 82
Db	301 SRLVVFYVEHTPWLFELPFILGVFGLWGFIRANIAWRKSTKFGKPYVILEV	360	Qy 65 DWRECKDKNRERHRINSKKKRSEAMETKSYIYDASWGLWVTLTGLASGALLGLIDIAAD 124
Qy	405 TIVATAVIAFPNPFYTRNTSELEKELTDGPLESSLCDYNDMNAKSVIYDIDPDR	464	Db 143 WMTDKEGICTEGVFNHEICWMSQQVIFEDRKCPENN 300
Db	361 LIVTAITIAFPNPFYTRNTSELEKELTDGPLESSLCDYNDMNAKSVIYDIDPDR	419	Qy 83 DWREKSRDRHREILSRSEKSTWALLHSVDAFSGWMMLLGLTAGSLAGLIDISH 142
Qy	465 AGIGYSAIWOLCLALIPLKIMTFEGKVPSCDFPSMAIGLAGRIVGIAVEOLAYY	524	Qy 125 WMTDKEGICLSALAMHNEOCWCWNSNETTFERDOPKQPKNTWAELITIGAEGPSYIMY 184
Db	420 AGAGVSSSAMWOLALIPLKIVITIFTFGMKIPSLEIFPSMAVGAIAGRILGVNGEOLAYH	479	Db 203 FMVWMAWLFSLAYLVLVRNFAFPYAGSGSIEPEIKTILSGFIRGLGKWLMIKITYLVL 262
Qy	525 HHDWTFIKEMCEVGADCTPGLYAMNGAACLGGVTRMTSLVWVIFELTGGIYIVPLM	584	Qy 245 AVASGLSLGREGPLGVHACCGNFSYLPKSYNEAKRREVLSASAAGSVAFGAPIG 304
Db	540 AAAMTSKWKWADALGREGYDAHTRLNGPFLEAKEFAHKTLANDVMKPRRNDDPLTVL	599	Db 323 GVLFSLSEEVSYVFPFLKTLMRSLFAAFLVAFTLRSNPGNRSVLYFVPHAPHLLEI 382
Qy	645 QDNMIVDDENMTHETSYGFPVIMSKESQRQGFAERDLTIAESARKKQGCVIGCSR	704	Qy 365 PFLIGVFGGLWGAFFIRANIAWRKSTKFGKPYVILEVITVATAVIAFPNPFRLN 424
Db	600 QDSMIVDVEDTTISPTSYGFPVIVSRESQRLVGFVLRDLSIISIENARKEODCVWSTSI	659	Db 383 PFLIGVFGGLWGAFFIRANIAWRKSTKFGKPYVILEVITVATAVIAFPNPFRLN 442
Qy	705 VCFQAOHTPSLPAESPRPLKRSILMSPTVTBHTPMELVWDIFRKLGRLQCLVTHNGRL	764	Qy 425 TSELTKELFTCGPTESSCDYNDMNAKSVIYDIDPDRAGIGYVSAIWQCLALIKI 484
Db	660 IYFTEHSPVPPVYATPLKURNTLDSPLTVTDLPMETVWDIFRKLGRLQCLVTHNGRL	719	Db 443 SSEMISELFNDGGLDSSKQDLYNDYNNWIK--GGNLPDRAGNGVYTAQMOLSLALIFKA 501
Qy	765 LGITTKKDILRHMATQANDPASIMN	791	Qy 485 IMTVTFGKIVPSGIFTPSMAIGLAGRIVGIAVEOLAYHHDWTFIKWCEVADCTP 544
Db	720 LGITTKKDILRHMATQANDPDSILFN	746	Db 502 VITITFGKIVPSGIFTPSMAIGLAGRIVGIAVEOLAYHHDWTFIKWCEVADCTP 561
RESULT 10			Qy 545 GLYAMGAAACGGYTRMIVSLVWVIFELTGGIYIVPLMAVMTSKWVDAFLGRGSYD 604
Q9PKW7	PRELIMINARY;	PRT;	Db 562 GLYAMGAAACGGYTRMIVSLVWVIFELTGGIYIVPLMAVMTSKWVDAFLGRGSYD 621
TD	09PKW7;		Qy 605 AHIRNGYPFDAKEEFTHTLADVMRPRRNDPLAVITQDNTMVTDDENMINETSYG 664
AC	01-MAY-2000 (TREMBLrel. 13, Created)		Db 622 AHTHNGYPFLEAKEEFSHKTLMADVMRPRRNDPLTATQDSMIVDTEAIISETYSG 681
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		Qy 665 FPVIMSKESQRVLEAFRLRROTELESARKKQEGVGSSVCFOHTPSLPAESPRPLK 724
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		Db 682 FPVIVSRESORLGMGVFLRDLITISESTARKKQEGVGSSVCFOHTPSLPAESPRPLK 741
DE	Chloride channel CIC-5.		Qy 725 RSTLDMSPFVTDHPMELVWDIFRKLGRLQCLVTHNGRLIGITKKDILRHMATQAND 784
GN	CIC-5.		Db 742 RAIMDLSPLSPFTDOPPMETVWDIFRKLGRLQCLVTHNGRLIGITKKDILRHMATQAND 801
OS	Xenopus laevis (African clawed frog).		Qy 785 PASTMEN 791
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db 802 PASTLFN 808
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RA	"Comparison of amphibian and human CIC-5"; Similarity of functional		
RT	properties and inhibition by external pH;"		
RT	J. Membr. Biol. 180:0-0(1999).		
RL	EMBL; AF0613904; ADD4497_1; -		
DR	InterPro; IPR000644; CBS_domain.		
DR	InterPro; IPR001807; C1-channel_volt.		
DR	InterPro; IPR001130; Tard_Dphase.		
Pfam	Pf00571; CBS; 2.		
PF00571; CBS; 2.			
RESULT 11			
O13080	PRELIMINARY;	PRT;	
ID	O13080		
AC	O13080;		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)		



QY	390	AGVGYTAMQALAAKFKVITITPFGMAMPSGLFIPSAVAGMAGRMGIGVGEQALH	449					
Db	525	HHDWFIFKKECEVGAACITGGLYANVGAACLGGVTRMTVSLWVVFELTGGLEYIVPJM	584					
Db	450	HHDWFIFKKECEVGAACLGGVTRMTVSLWVVFELTGGLEYIVPJM	509					
Db	585	AAVMTSKWADAFGREGKGYIPEAHIRINGYPLDVKDFEHTLADVMRRRNDPLAVL	644					
Qy	510	AAVMTSKWADAFGREGKGYIPEAHIRINGYPLDVKDFEHTLADVMRRRNDPLAVL	569					
Db	570	QDSMIVEDVETLILIKEIDYNGPPVLSRSDERLIGFAQRRELLAIKWARQEGIVSNL	629					
Qy	645	QDNMTVDIENINNETSYNCPVIMSKESORLVGALARLITIAESARKKQEGIVGSSR	704					
Db	630	VCFAGHTPSPAESRPLKRSILMSPFVTDHPMEVWDIRKLGLRQCLVTHNGSL	764					
Db	690	MYFTERPEPLANSPPHLKLRLINLSPFVTDHPMETVUDFIRKLGLRQCLVTRSGRL	689					
Qy	765	LGIIKKDILRHMAOTANQDPMASIN	791					
Db	690	LGITTKDVRHMAQMANQDPESIMEN	716					
RESULT	13							
Q9PUT5								
ID		PRELIMINARY;	PRT;					
AC			840 AA.					
DT	01-MAY-2000	(TREMBLrel.	13, Created)					
DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)					
DE	01-JUN-2002	(TREMBLrel.	21, Last annotation update)					
DE	Chloride channel CIC-3.							
DE	Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;							
OC	Ocichthyes; Acanthopterygii; Perciformes; Labroidei;							
OX	NCBI_TaxID=8127;							
RN								
RP								
SEQUENCE FROM N.A.								
RX	MEDLINE=95185316;							
RA	Miyazaki H., Uchida S., Takei Y., Hirano T., Marumo F., Sasaki S.;							
RT	"Molecular cloning of CLC chloride channels in Oreochromis mossambicus and their functional complementation of yeast CLC gene mutant.;"							
RL	Biochem. Biophys. Res. Commun. 255:175-181(1999).							
DR	EMBL:AF182216; AAD56389; 1; -.							
DR	InterPro: IPR000644; CBS:domain.							
DR	InterPro: IPR001807; CL-channel_volt.							
PFam: PF00571; CBS; 2.								
PRM: PF00654; voltage,CNC; 1.								
PRM: PR00762; CLchannel.								
PRM: SMART; SW00116; CBS; 2.								
DR	SMART; SW00116; CBS; 2.							
SQ	SEQUENCE	840 AA;	92293 MW;					
SQ	81B9996E446F9605	CRC64;						
Query	Match	72.6%	Score	3031;	DB	13;	Length	840;
Best Local Similarity	71.8%	;	Pred.	No.	5.	8e-237;		
Matches	562;	Conservative	103;	Mismatches	108;	Indels	10;	Gaps
Qy	16	DNTP-----DRELHKRGTHMTNGSINSTHLDLDEPIRGVGTDPHTIDWREK	70					
Db	61	DDVPPLSSGTYEEH-NGSRTAGINGS--GPSRVDPDPLPVEGTEDFNTIDWREN	117					
Qy	71	CKDRERRRNRSKKESEMTPKSLYDAGSWLWVLTGLASGALAGLIDIAWDWTIK	130					
Db	118	SKDRDRHREITNSKROSTVALLHSIDASFGWLMLLVGLMSGALAGGIDISAIWMTDK	177					
Qy	131	EGICLALSALWNHEOCWGSGNETTEFEERDKCPQWTKTWAELITIGQAEGPSGYIMNYIMYFW	190					
Db	178	GGLCRGFWNHECWCWLSNETTQERDRCPQWMSWAEITIGKSEGPFAYIVNLYFW	237					
Qy	191	ALSFAPLAVSLVKYFAPYAGSGSGPEIKITLSGIFTIGKWTMIKITLTLAVASGL	250					
Db	238	ALMFSFLAVLVRAPAGGSGSGPEIKITLSGIFTIGKWTMIKITLTLAVASGL	297					
Qy								
Db								
RESULT	14							
Q9VUV1								
ID		PRELIMINARY;	PRT;					
AC			732 AA.					
DT	01-MAY-2000	(TREMBLrel.	13, Created)					
DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)					
DT	01-JUN-2002	(TREMBLrel.	21, Last annotation update)					
DE	CG5284	protein.						
OS	Drosophila melanogaster (Fruit fly).							
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;							
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;							
OC	Ephydriidae; Drosophilidae; Drosophila.							
OX	NCBI_TaxID=7227;							
RN								
RP								
SEQUENCE FROM N.A.								
RX	STRAIN=BERKELEY;							
RX	MEDLINE=20196006;							
RA	Adams M. D., Celniker S. E., Holt R. A., Evans C. A., Gocayne J. D.,							
RA	Amanatides P. G., Scherer S. E., Li P. W., Hoskins R. A., Galle R. F.,							
RA	George R. A., Lewis S. E., Richards S. M., Ashburner M., Henderson S. N.,							
RA	Sutton G. G., Wortman J. R., Yandell M. D., Zhang Q., Chen L. X.,							
RA	Brandon R. C., Rogers Y.-H. C., Blazej R. G., Champe M., Pfeiffer B. D.,							
RA	Wan K. H., Doyle C., Baxter E. G., Helt G., Nelson C. R., Miklos G. L. G.,							
RA	Abrial J. F., Abyzov A., An H.-J., Andrews P.-Fannoch C., Baldwin D.,							
RA	Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M.,							
RA	Beeson K. Y., Benos P. V., Berman B. P., Bhattachari S., Bolshakov S.,							
RA	Borkova D., Botchan M. R., Bouck J., Brockstein P., Brotman P.,							
RA	Burtis K. C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,							
RA	Cherry J. M., Cawley S., Dahike C., Davenport L. B., Davies P.,							
RA	de Pablos B., Delcher A., Deng Z., Mays A. D., Dew I., Dietz S. M.,							



QY 115 LAGLIDIADWMTDLKEGICLALSALWYNHQCNCQSNET'FEERDCKCPOWRTAELIIGQA 174  
 Db 128 TAGIDIGARWMSDLKIGWCADREWLDRHCCNSNDPFIKD-DDCKAWTKWPWML-NY 184  
 QY 175 EGPSSYI--MNYDMYIWALSPRAFLAVASLKVFAPIYACGSGIPEIKTLSGFIRGYLG 231  
 Db 185 YNSSSPFLFLEWIFIYIGWAVAMSTLAVLFVKIFAPYACGSGIPEIKCILSGFIRGYLG 244  
 QY 232 KWTLMIKITLTLAVASGLGEGPLVHACCGNISLFPKSYNEAKKEVLSAS 291  
 Db 245 KWTMITSKVLGILSSASGLGEGPLVHACCGNISLFPKSYNEAKKEVLSAS 304  
 QY 292 AAGVSVAAGPIGGVLFSLEEVSYVPPKTLWRSFAALVAFVDRSTNPFGNSRLVLFY 351  
 Db 305 AAGVSVAAGPIGGVLFSLEASYVPLKTMWSFCAVAGTILRFNPFGSNQTSLFH 364  
 QY 352 VEYHMPWYLFLFBFTLGLGVFGGLWGAFFRANIAWCRRRSKR-FGKPVLPVITIVAI 410  
 Db 365 VDYMWKWIFIYLPFAILGLFGGIISLFFANIRWSFRKNSKMLGGNPYEVMLTLY 424  
 QY 411 TAVIAFPNPyTRNTSELKELEPDC-OPLESSLCYRNDMASKIVDDIPRPRAGIV 469  
 Db 425 TAATSYFNFTRASQSMQDCEQDIDSLCDONKAISI----- 468  
 QY 470 YSATWQCLALIKIMUVFTFGIKVPSCLFPSMAIGAIAGRIVGAVEQL----AY 523  
 Db 469 --AFGQLWALIKFVITLFTFGIKVPGFLFVSIQMGIAIGRITLGITWDQIFRAVQATP 526  
 QY 524 YHHDWIFIFNEWCEVGDCTPGLYAMWGAACIUGGVTRMTVSLVVTVELTGLEYVPL 583  
 Db 527 GHSDYFT--CQIGKDCVMPGLYAMVGAARAVLGGVTRMTVSLVIMFELTGSLEFTVPT 582  
 QY 584 MAAYTMSKHWGDAFREGREGYEAHILNGLYPEFLDAKEEETHTTLAADVNRP----- 633  
 Db 583 MVATMFSKVGDGTSKMGYEAHILNGLYPEFLDSKGEPYSTVASSQMRPSIHRQVADEM 642  
 QY 634 -----RRNUPPLAVLTQDMNTVDDIENMINETSYNGFVIMSKEQRLVGFALRDLTIA 688  
 Db 643 SMDLRELKNELSVTIESGMLGDLLESLRLQDGFNPVWVSONSMHUGFTRRDILLA 702  
 QY 689 IESARKKOEKGIVESSRVEFAQHPTSLPAPSPRPLKRLSTLDMSPPFTVTDHTPMEVIVDIF 748  
 Db 703 LHPAKTQPYWNTSIAVFSGDPAMPGGPAPLRLRKTLDMAPMTYDQTPMETHVDMF 762  
 QY 749 RKUGLRQCLVTHNGRLGIGITKDLRHMATQ 783  
 Db 763 RKUGLRHVLVTKNGKVLGITKDLQMRNKNSQ 797

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